

SEQUENCE LISTING

<110> Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.

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<140> PCT/EP2005/050131

<141> 2005-01-13

<150> 04000847.6

<151> 2004-01-16

<150> 04017928.5

<151> 2004-07-29

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<170> PatentIn Ver. 2.1

<210> 1

<211> 1785

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:

PMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

<220>

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<222> (1)..(1785)

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<221> N_region

<222> (1)..(21)

<223> immunogloblin kappa chain leader sequence

<400> 1

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Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro	
1				5					10					15		

ggt	tcc	act	ggt	gac	tct	aga	atg	gtc	cag	gcc	tcg	atg	agg	agc	cca	96
Gly	Ser	Thr	Gly	Asp	Ser	Arg	Met	Val	Gln	Ala	Ser	Met	Arg	Ser	Pro	
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aat	atg	gag	acg	ttc	aaa	cag	cag	aag	gtg	gag	gac	ttt	tat	gat	att	144
Asn	Met	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Glu	Asp	Phe	Tyr	Asp	Ile	
		35				40					45					

gga	gag	gag	ctg	ggc	agt	ggc	cag	ttt	gcc	atc	gtg	aag	aag	tgc	cgg	192
Gly	Glu	Glu	Leu	Gly	Ser	Gly	Gln	Phe	Ala	Ile	Val	Lys	Lys	Cys	Arg	
	50					55					60					

gag aag agc acg ggg ctg gag tat gca gcc aag ttc att aag aag agg	240
Glu Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg	
65 70 75 80	
cag agc cgg gcc agc cgt cgg ggc gtg tgc cgg gag gaa atc gag cgg	288
Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg	
85 90 95	
gag gtg agc atc ctg cgg cag gtg ctg cac ccc aac atc atc acg ctg	336
Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu	
100 105 110	
cac gac gtc tat gag aac cgc acc gac gtg gtg ctc atc ctt gag cta	384
His Asp Val Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu	
115 120 125	
gtg tcc gga gga gaa ctg ttt gat ttc ctg gcc cag aag gag tcg tta	432
Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu	
130 135 140	
agt gag gag gaa gcc acc agc ttc att aag cag atc ctg gat ggg gtg	480
Ser Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val	
145 150 155 160	
aat tac ctt cac aca aag aaa att gct cac ttt gat ctc aag cca gaa	528
Asn Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu	
165 170 175	
aac atc atg ttg tta gac aag aat atc cca att cca cac atc aag ctg	576
Asn Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu	
180 185 190	
att gac ttt ggc ctg gct cac gaa ata gaa gat gga gtt gaa ttt aaa	624
Ile Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys	
195 200 205	
aac att ttt ggg aca cct gaa ttt gtt gct cca gaa atc gtg aac tat	672
Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr	
210 215 220	
gag cca ctg gga ctg gag gcc gac atg tgg agc att gga gtc atc acc	720
Glu Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr	
225 230 235 240	
tat atc ctt cta agt gga gcg tcc ccc ttc ctg gga gac aca aaa caa	768
Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln	
245 250 255	
gaa acc ctg gca aat atc act gct gtg agt tac gac ttt gat gag gaa	816
Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu	
260 265 270	
ttc ttc agc cag aca agc gag ctg gcc aag gac ttc att cgg aag ctt	864
Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu	
275 280 285	

ctt gtg aaa gag acc cgg aaa cgg ctt acc atc caa gag gct ctc aga	912
Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg	
290 295 300	
cat ccc tgg atc gga tcc aaa cta gct gag cac gaa ggt gac gcg gcc	960
His Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Gly Asp Ala Ala	
305 310 315 320	
cag ccg gcc atg gcc cag gtc aag ctg cag gag tca ggg act gaa ctg	1008
Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr Glu Leu	
325 330 335	
gca aag cct ggg gcc gca gtg aag atg tcc tgc aag gct tct ggc tac	1056
Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser Gly Tyr	
340 345 350	
acc ttt act gac tac tgg atg cac tgg gtt aaa cag agg cct gga cag	1104
Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln	
355 360 365	
ggg ctg gaa tgg att gga tac att aat cct aac act gct tat act gac	1152
Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr Thr Asp	
370 375 380	
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Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser	
385 390 395 400	
tcc agc aca gcc tac atg caa ctg cgc agc ctg acc tct gag gat tct	1248
Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser	
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gca gtc tat tac tgt gca aaa aag aca act cag act acg tgg ggg ttt	1296
Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp Gly Phe	
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cct ttt tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gga ggc	1344
Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly	
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Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu	
450 455 460	
acc cag tct cca aaa tcc atg gcc atg tca gtc gga gag agg gtc acc	1440
Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg Val Thr	
465 470 475 480	
ttg agc tgc aag gcc agt gag aat gtg gat tct ttt gtt tcc tgg tat	1488
Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser Trp Tyr	
485 490 495	
caa cag aaa cca ggc cag tct cct aaa ctg ctg ata tac ggg gcc tcc	1536
Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser	
500 505 510	

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Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala
      530                      535                      540

gat tat cac tgt gga cag aat tac agg tat ccg ctc acg ttc ggt gct      1680
Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe Gly Ala
      545                      550                      555                      560

ggc acc aag ctg gaa atc aaa cgg gcg gcc gca ggg ccc gaa caa aaa      1728
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      565                      570                      575

ctc atc tca gaa gag gat ctg aat agc gcc gtc gac cat cat cat cat      1776
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cat cat tga
His His
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<210> 2

<211> 594

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:

pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

<400> 2

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Asn Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile
      35              40              45
Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg
      50              55              60
Glu Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg
      65              70              75              80
Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg
      85              90              95
Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu
      100             105             110
His Asp Val Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu
      115             120             125
Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu
      130             135             140
Ser Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val
      145             150             155             160
Asn Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu
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Asn Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu

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$\langle 210 \rangle$ 3

<211> 1794
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<213> Artificial Sequence

<220>
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pMS-(Ki-4-DAPK2')-II/G ORF

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<222> (1)..(1794)

<220>
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<222> (1)..(21)
<223> immunoglobulin kappa chain leader sequence

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ggt tcc act ggt gac gcg gcc cag ccg gcc atg gcc cag gtc aag ctg 96
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu
20 25 30
cag gag tca ggg act gaa ctg gca aag cct ggg gcc gca gtg aag atg 144
Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met
35 40 45
tcc tgc aag gct tct ggc tac acc ttt act gac tac tgg atg cac tgg 192
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp
50 55 60
gtt aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att aat 240
Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
65 70 75 80
cct aac act gct tat act gac tac aat cag aaa ttc aag gac aag gcc 288
Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala
85 90 95
aca ttg act gca gac aaa tcc tcc agc aca gcc tac atg caa ctg cgc 336
Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg
100 105 110
agc ctg acc tct gag gat tct gca gtc tat tac tgt gca aaa aag aca 384
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr
115 120 125
act cag act acg tgg ggg ttt cct ttt tgg ggc caa ggg acc acg gtc 432
Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val
130 135 140
acc gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt 480
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

145											150											155											160	
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Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met																																		
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tca gtc gga gag agg gtc acc ttg agc tgc aag gcc agt gag aat gtg											576																							
Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val																																		
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gat tct ttt gtt tcc tgg tat caa cag aaa cca ggc cag tct cct aaa											624																							
Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys																																		
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ctg ctg ata tac ggg gcc tcc aac cgg tac act ggg gtc ccc gat cgc											672																							
Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg																																		
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ttc gca ggc agt gga tct gga aga gat ttc act ctg acc atc agc agt											720																							
Phe Ala Gly Ser Gly Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser																																		
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Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg																																		
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tat ccg ctc acg ttc ggt gct ggc acc aag ctg gaa atc aaa cgg gcg											816																							
Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala																																		
										260											265											270		
gcc gca ctc gag tct aga atg gtc cag gcc tcg atg agg agc cca aat											864																							
Ala Ala Leu Glu Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro Asn																																		
										275											280											285		
atg gag acg ttc aaa cag cag aag gtg gag gac ttt tat gat att gga											912																							
Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly																																		
										290											295											300		
gag gag ctg ggc agt ggc cag ttt gcc atc gtg aag aag tgc cgg gag											960																							
Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu																																		
										305											310											315		
aag agc acg ggg ctg gag tat gca gcc aag ttc att aag aag agg cag											1008																							
Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln																																		
										325											330											335		
agc cgg gcc agc cgt cgg ggc gtg tgc cgg gag gaa atc gag cgg gag											1056																							
Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg Glu																																		
										340											345											350		
gtg agc atc ctg cgg cag gtg ctg cac ccc aac atc atc acg ctg cac											1104																							
Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu His																																		
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gac ctc tat gag aac cgc acc gac gtg gtg ctc atc ctt gag cta gtg											1152																							
Asp Leu Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu Val																																		

370	375	380	
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385	390	395	400
gag gag gaa gcc acc agc ttc att aag cag atc ctg gat ggg gtg aat			1248
Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn			
	405	410	415
tac ctt cac aca aag aaa att gct cac ttt gat ctc aag cca gaa aac			1296
Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn			
	420	425	430
atc atg ttg tta gac aag aat atc cca att cca cac atc aag ctg att			1344
Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile			
	435	440	445
gac ttt ggc ctg gct cac gaa ata gaa gat gga gtt gaa ttt aaa aac			1392
Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn			
	450	455	460
att ttt ggg aca cct gaa ttt gtt gct cca gaa atc gtg aac tat gag			1440
Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu			
	465	470	480
cca ctg gga ctg gag gcc gac atg tgg agc att gga gtc atc acc tat			1488
Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr			
	485	490	495
atc ctt cta agt gga gcg tcc ccc ttc ctg gga gac aca aaa caa gaa			1536
Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu			
	500	505	510
acc ctg gca aat atc act gct gtg agt tac gac ttt gat gag gaa ttc			1584
Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu Phe			
	515	520	525
ttc agc cag aca agc gag ctg gcc aag gac ttc att cgg aag ctt ctt			1632
Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu			
	530	535	540
gtg aaa gag acc cgg aaa cgg ctt acc atc caa gag gct ctc aga cat			1680
Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His			
	545	550	560
ccc tgg atc gga tcc aaa cta gct gag cac gaa ttt cga gga ggg ccc			1728
Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Phe Arg Gly Gly Pro			
	565	570	575
gaa caa aaa ctc atc tca gaa gag gat ctg aat agc gcc gtc gac cat			1776
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His			
	580	585	590
cat cat cat cat cat tga			1794
His His His His His			

595

<210> 4
 <211> 597
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:
 pMS-(Ki-4-DAPK2')-II/G ORF

<400> 4
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 35 40 45
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp
 50 55 60
 Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 65 70 75 80
 Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala
 85 90 95
 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg
 100 105 110
 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr
 115 120 125
 Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val
 130 135 140
 Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 145 150 155 160
 Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met
 165 170 175
 Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val
 180 185 190
 Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
 195 200 205
 Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
 210 215 220
 Phe Ala Gly Ser Gly Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser
 225 230 235 240
 Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg
 245 250 255
 Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala
 260 265 270
 Ala Ala Leu Glu Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro Asn
 275 280 285
 Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly
 290 295 300
 Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu
 305 310 315 320
 Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln
 325 330 335
 Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg Glu
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 Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu His

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385          390          395          400
Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn
          405          410          415
Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn
          420          425          430
Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile
          435          440          445
Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn
          450          455          460
Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
465          470          475          480
Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
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Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu
          500          505          510
Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu Phe
          515          520          525
Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu
          530          535          540
Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His
545          550          555          560
Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Phe Arg Gly Gly Pro
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Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His
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<211> 3102

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PMT-Ki-4
(scFv)-eEF-2K ORF

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<222> (1)..(3102)

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<221> N_region

<222> (2)..(22)

<223> pelB leader sequence

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His His Ser Ser Gly His Ile Asp Asp Asp Asp Lys His Met Lys Leu	
35 40 45	
atg gcc cag ccg gcc atg gcc cag gtc aag ctg cag gag tca ggg act	192
Met Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr	
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gaa ctg gca aag cct ggg gcc gca gtg aag atg tcc tgc aag gct tct	240
Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser	
65 70 75 80	
ggc tac acc ttt act gac tac tgg atg cac tgg gtt aaa cag agg cct	288
Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro	
85 90 95	
gga cag ggt ctg gaa tgg att gga tac att aat cct aac act gct tat	336
Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr	
100 105 110	
act gac tac aat cag aaa ttc aag gac aag gcc aca ttg act gca gac	384
Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp	
115 120 125	
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Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu	
130 135 140	
gat tct gca gtc tat tac tgt gca aaa aag aca act cag act acg tgg	480
Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp	
145 150 155 160	
ggg ttt cct ttt tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt	528
Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly	
165 170 175	
gga ggc ggt tca ggc gga ggt ggc tct ggc ggt ggc gga tcg gac att	576
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile	
180 185 190	
gtg ctg acc cag tct cca aaa tcc atg gcc atg tca gtc gga gag agg	624
Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg	
195 200 205	
gtc acc ttg agc tgc aag gcc agt gag aat gtg gat tct ttt gtt tcc	672
Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser	
210 215 220	
tgg tat caa cag aaa cca ggc cag tct cct aaa ctg ctg ata tac ggg	720
Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly	
225 230 235 240	

gcc tcc aac cgg tac act ggg gtc ccc gat cgc ttc gca ggc agt gga	768
Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly	
245 250 255	
tct gga aga gat ttc act ctg acc atc agc agt gtg cag gct gaa gac	816
Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp	
260 265 270	
ctt gca gat tat cac tgt gga cag aat tac agg tat ccg ctc acg ttc	864
Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe	
275 280 285	
ggg gct ggc acc aag ctg gaa atc aaa cgg gcg gcc gca gag ctc ggc	912
Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu Leu Gly	
290 295 300	
gga ggt ggc tct atg gca gac gaa gat ctc atc ttc cgc ctg gaa ggc	960
Gly Gly Gly Ser Met Ala Asp Glu Asp Leu Ile Phe Arg Leu Glu Gly	
305 310 315 320	
gtt gat ggc ggc cag tcc ccc cga gct ggc cat gat ggt gat tct gat	1008
Val Asp Gly Gly Gln Ser Pro Arg Ala Gly His Asp Gly Asp Ser Asp	
325 330 335	
ggg gac agc gac gat gag gaa ggt tac ttc atc tgc ccc atc acg gat	1056
Gly Asp Ser Asp Asp Glu Glu Gly Tyr Phe Ile Cys Pro Ile Thr Asp	
340 345 350	
gac cca agc tcg aac cag aat gtc aat tcc aag gtt aat aag tac tac	1104
Asp Pro Ser Ser Asn Gln Asn Val Asn Ser Lys Val Asn Lys Tyr Tyr	
355 360 365	
agc aac cta aca aaa agt gag cgg tat agc tcc agc ggg tcc ccg gca	1152
Ser Asn Leu Thr Lys Ser Glu Arg Tyr Ser Ser Ser Gly Ser Pro Ala	
370 375 380	
aac tcc ttc cac ttc aag gaa gcc tgg aag cac gca atc cag aag gcc	1200
Asn Ser Phe His Phe Lys Glu Ala Trp Lys His Ala Ile Gln Lys Ala	
385 390 395 400	
aag cac atg ccc gac ccc tgg gct gag ttc cac ctg gaa gat att gcc	1248
Lys His Met Pro Asp Pro Trp Ala Glu Phe His Leu Glu Asp Ile Ala	
405 410 415	
acc gaa cgt gct act cga cac agg tac aac gcc gtc acc ggg gaa tgg	1296
Thr Glu Arg Ala Thr Arg His Arg Tyr Asn Ala Val Thr Gly Glu Trp	
420 425 430	
ctg gat gat gaa gtt ctg atc aag atg gca tct cag ccc ttc ggc cga	1344
Leu Asp Asp Glu Val Leu Ile Lys Met Ala Ser Gln Pro Phe Gly Arg	
435 440 445	
gga gca atg agg gag tgc ttc cgg acg aag aag ctc tcc aac ttc ttg	1392
Gly Ala Met Arg Glu Cys Phe Arg Thr Lys Lys Leu Ser Asn Phe Leu	
450 455 460	

cat gcc cag cag tgg aag ggc gcc tcc aac tac gtg gcg aag cgc tac	1440
His Ala Gln Gln Trp Lys Gly Ala Ser Asn Tyr Val Ala Lys Arg Tyr	
465 470 475 480	
atc gag ccc gta gac cgg gat gtg tac ttt gag gac gtg cgt cta cag	1488
Ile Glu Pro Val Asp Arg Asp Val Tyr Phe Glu Asp Val Arg Leu Gln	
485 490 495	
atg gag gcc aag ctc tgg ggg gag gag tat aat cgg cac aag ccc ccc	1536
Met Glu Ala Lys Leu Trp Gly Glu Tyr Asn Arg His Lys Pro Pro	
500 505 510	
aag cag gtg gac atc atg cag atg tgc atc atc gag ctg aag gac aga	1584
Lys Gln Val Asp Ile Met Gln Met Cys Ile Ile Glu Leu Lys Asp Arg	
515 520 525	
ccg ggc aag ccc ctc ttc cac ctg gag cac tac atc gag ggc aag tac	1632
Pro Gly Lys Pro Leu Phe His Leu Glu His Tyr Ile Glu Gly Lys Tyr	
530 535 540	
atc aag tac aac tcc aac tct ggc ttt gtc cgc gat gac aac atc cgc	1680
Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Arg Asp Asp Asn Ile Arg	
545 550 555 560	
ctg acg ccg cag gcc ttc agc cac ttc act ttt gag cgt tcc ggc cat	1728
Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His	
565 570 575	
cag ctg ata gtg gtg gac atc cag gga gtt ggg gat ctc tac act gac	1776
Gln Leu Ile Val Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp	
580 585 590	
cca cag atc cac acg gag acg ggc act gac ttt gga gac ggc aac cta	1824
Pro Gln Ile His Thr Glu Thr Gly Thr Asp Phe Gly Asp Gly Asn Leu	
595 600 605	
ggt gtc cgc ggg atg gcg ctc ttc ttc tac tct cat gcc tgc aac cgg	1872
Gly Val Arg Gly Met Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg	
610 615 620	
att tgc gag agc atg ggc ctt gct ccc ttt gac ctc tcg ccc cgg gag	1920
Ile Cys Glu Ser Met Gly Leu Ala Pro Phe Asp Leu Ser Pro Arg Glu	
625 630 635 640	
agg gat gca gtg aat cag aac acc aag ctg ctg caa tca gcc aag acc	1968
Arg Asp Ala Val Asn Gln Asn Thr Lys Leu Leu Gln Ser Ala Lys Thr	
645 650 655	
atc ttg aga gga aca gag gaa aaa tgt ggg agc ccc cga gta agg acc	2016
Ile Leu Arg Gly Thr Glu Glu Lys Cys Gly Ser Pro Arg Val Arg Thr	
660 665 670	
ctc tct ggg agc cgg cca ccc ctg ctc cgt ccc ctt tca gag aac tct	2064
Leu Ser Gly Ser Arg Pro Pro Leu Leu Arg Pro Leu Ser Glu Asn Ser	
675 680 685	

gga gac gag aac atg agc gac gtg acc ttc gac tct ctc cct tct tcc	2112
Gly Asp Glu Asn Met Ser Asp Val Thr Phe Asp Ser Leu Pro Ser Ser	
690 695 700	
cca tct tcg gcc aca cca cac agc cag aag cta gac cac ctc cat tgg	2160
Pro Ser Ser Ala Thr Pro His Ser Gln Lys Leu Asp His Leu His Trp	
705 710 715 720	
cca gtc ttc agt gac ctc gat aac atg gca tcc aga gac cat gat cat	2208
Pro Val Phe Ser Asp Leu Asp Asn Met Ala Ser Arg Asp His Asp His	
725 730 735	
cta gac aac cac cgg gag tct gag aat agt ggg gac agc gga tac ccc	2256
Leu Asp Asn His Arg Glu Ser Glu Asn Ser Gly Asp Ser Gly Tyr Pro	
740 745 750	
agt gag aag cgg ggt gag ctg gat gac cct gag ccc cga gaa cat ggc	2304
Ser Glu Lys Arg Gly Glu Leu Asp Asp Pro Glu Pro Arg Glu His Gly	
755 760 765	
cac tca tac agt aat cgg aag tac gag tct gac gaa gac agc ctg ggc	2352
His Ser Tyr Ser Asn Arg Lys Tyr Glu Ser Asp Glu Asp Ser Leu Gly	
770 775 780	
agc tct gga cgg gta tgt gta gag aag tgg aat ctc ctc aac tcc tcc	2400
Ser Ser Gly Arg Val Cys Val Glu Lys Trp Asn Leu Leu Asn Ser Ser	
785 790 795 800	
cgc ctc cac ctg ccg agg gct tcg gcc gtg gcc ctg gaa gtg caa agg	2448
Arg Leu His Leu Pro Arg Ala Ser Ala Val Ala Leu Glu Val Gln Arg	
805 810 815	
ctt aat gct ctg gac ctc gaa aag aaa atc ggg aag tcc att ttg ggg	2496
Leu Asn Ala Leu Asp Leu Glu Lys Lys Ile Gly Lys Ser Ile Leu Gly	
820 825 830	
aag gtc cat ctg gcc atg gtg cgc tac cac gag ggt ggg cgc ttc tgc	2544
Lys Val His Leu Ala Met Val Arg Tyr His Glu Gly Arg Phe Cys	
835 840 845	
gag aag ggc gag gag tgg gac cag gag tcg gct gtc ttc cac ctg gag	2592
Glu Lys Gly Glu Glu Trp Asp Gln Glu Ser Ala Val Phe His Leu Glu	
850 855 860	
cac gca gcc aac ctg ggc gag ctg gag gcc atc gtg ggc ctg gga ctc	2640
His Ala Ala Asn Leu Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu	
865 870 875 880	
atg tac tcg cag ttg cct cat cac atc cta gcc gat gtc tct ctg aag	2688
Met Tyr Ser Gln Leu Pro His His Ile Leu Ala Asp Val Ser Leu Lys	
885 890 895	
gag aca gaa gag aac aaa acc aaa gga ttt gat tac tta cta aag gcc	2736
Glu Thr Glu Glu Asn Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala	
900 905 910	

gct gaa gct ggc gac agg cag tcc atg atc cta gtg gcg cga gct ttt 2784
Ala Glu Ala Gly Asp Arg Gln Ser Met Ile Leu Val Ala Arg Ala Phe
915 920 925

gac tct ggc cag aac ctc agc ccg gac agg tgc caa gac tgg cta gag 2832
Asp Ser Gly Gln Asn Leu Ser Pro Asp Arg Cys Gln Asp Trp Leu Glu
930 935 940

gcc ctg cac tgg tac aac act gcc ctg gag atg acg gac tgt gat gag 2880
Ala Leu His Trp Tyr Asn Thr Ala Leu Glu Met Thr Asp Cys Asp Glu
945 950 955 960

ggc ggt gag tac gac gga atg cag gac gag ccc cgg tac atg atg ctg 2928
Gly Gly Glu Tyr Asp Gly Met Gln Asp Glu Pro Arg Tyr Met Met Leu
965 970 975

gcc agg gag gcc gag atg ctg ttc aca gga ggc tac ggg ctg gag aag 2976
Ala Arg Glu Ala Glu Met Leu Phe Thr Gly Gly Tyr Gly Leu Glu Lys
980 985 990

gac ccg cag aga tca ggg gac ttg tat acc cag gca gca gag gca gcg 3024
Asp Pro Gln Arg Ser Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala
995 1000 1005

atg gaa gcc atg aag ggc cga ctg gcc aac cag tac tac caa aag gct 3072
Met Glu Ala Met Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys Ala
1010 1015 1020

gaa gag gcc tgg gcc cag atg gag gag taa 3102
Glu Glu Ala Trp Ala Gln Met Glu Glu
1025 1030

<210> 6

<211> 1033

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pMT-Ki-4
(scFv)-eEF-2K ORF

<400> 6

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1 5 10 15
Ala Gln Pro Ala Met Ala Met Gly His His His His His His His
20 25 30
His His Ser Ser Gly His Ile Asp Asp Asp Asp Lys His Met Lys Leu
35 40 45
Met Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr
50 55 60
Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser
65 70 75 80
Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro
85 90 95
Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr
100 105 110

Thr	Asp	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ala	Asp
		115					120					125			
Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Arg	Ser	Leu	Thr	Ser	Glu
	130					135					140				
Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Lys	Thr	Thr	Gln	Thr	Thr	Trp
145					150					155					160
Gly	Phe	Pro	Phe	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly
				165					170					175	
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile
			180					185					190		
Val	Leu	Thr	Gln	Ser	Pro	Lys	Ser	Met	Ala	Met	Ser	Val	Gly	Glu	Arg
		195					200					205			
Val	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Glu	Asn	Val	Asp	Ser	Phe	Val	Ser
	210					215					220				
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly
225					230					235					240
Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Ala	Gly	Ser	Gly
				245					250					255	
Ser	Gly	Arg	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp
			260					265						270	
Leu	Ala	Asp	Tyr	His	Cys	Gly	Gln	Asn	Tyr	Arg	Tyr	Pro	Leu	Thr	Phe
		275					280					285			
Gly	Ala	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Glu	Leu	Gly
	290					295					300				
Gly	Gly	Gly	Ser	Met	Ala	Asp	Glu	Asp	Leu	Ile	Phe	Arg	Leu	Glu	Gly
305					310					315					320
Val	Asp	Gly	Gly	Gln	Ser	Pro	Arg	Ala	Gly	His	Asp	Gly	Asp	Ser	Asp
				325					330					335	
Gly	Asp	Ser	Asp	Asp	Glu	Glu	Gly	Tyr	Phe	Ile	Cys	Pro	Ile	Thr	Asp
		340						345					350		
Asp	Pro	Ser	Ser	Asn	Gln	Asn	Val	Asn	Ser	Lys	Val	Asn	Lys	Tyr	Tyr
		355					360					365			
Ser	Asn	Leu	Thr	Lys	Ser	Glu	Arg	Tyr	Ser	Ser	Ser	Gly	Ser	Pro	Ala
	370					375					380				
Asn	Ser	Phe	His	Phe	Lys	Glu	Ala	Trp	Lys	His	Ala	Ile	Gln	Lys	Ala
385					390					395					400
Lys	His	Met	Pro	Asp	Pro	Trp	Ala	Glu	Phe	His	Leu	Glu	Asp	Ile	Ala
				405					410					415	
Thr	Glu	Arg	Ala	Thr	Arg	His	Arg	Tyr	Asn	Ala	Val	Thr	Gly	Glu	Trp
			420					425					430		
Leu	Asp	Asp	Glu	Val	Leu	Ile	Lys	Met	Ala	Ser	Gln	Pro	Phe	Gly	Arg
	435						440					445			
Gly	Ala	Met	Arg	Glu	Cys	Phe	Arg	Thr	Lys	Lys	Leu	Ser	Asn	Phe	Leu
	450					455					460				
His	Ala	Gln	Gln	Trp	Lys	Gly	Ala	Ser	Asn	Tyr	Val	Ala	Lys	Arg	Tyr
465					470					475					480
Ile	Glu	Pro	Val	Asp	Arg	Asp	Val	Tyr	Phe	Glu	Asp	Val	Arg	Leu	Gln
				485					490					495	
Met	Glu	Ala	Lys	Leu	Trp	Gly	Glu	Glu	Tyr	Asn	Arg	His	Lys	Pro	Pro
			500					505					510		
Lys	Gln	Val	Asp	Ile	Met	Gln	Met	Cys	Ile	Ile	Glu	Leu	Lys	Asp	Arg
	515						520					525			
Pro	Gly	Lys	Pro	Leu	Phe	His	Leu	Glu	His	Tyr	Ile	Glu	Gly	Lys	Tyr
	530					535					540				
Ile	Lys	Tyr	Asn	Ser	Asn	Ser	Gly	Phe	Val	Arg	Asp	Asp	Asn	Ile	Arg
545					550					555					560

Leu	Thr	Pro	Gln	Ala	Phe	Ser	His	Phe	Thr	Phe	Glu	Arg	Ser	Gly	His		
				565					570					575			
Gln	Leu	Ile	Val	Val	Asp	Ile	Gln	Gly	Val	Gly	Asp	Leu	Tyr	Thr	Asp		
			580					585					590				
Pro	Gln	Ile	His	Thr	Glu	Thr	Gly	Thr	Asp	Phe	Gly	Asp	Gly	Asn	Leu		
		595					600					605					
Gly	Val	Arg	Gly	Met	Ala	Leu	Phe	Phe	Tyr	Ser	His	Ala	Cys	Asn	Arg		
	610					615					620						
Ile	Cys	Glu	Ser	Met	Gly	Leu	Ala	Pro	Phe	Asp	Leu	Ser	Pro	Arg	Glu		
625					630					635					640		
Arg	Asp	Ala	Val	Asn	Gln	Asn	Thr	Lys	Leu	Leu	Gln	Ser	Ala	Lys	Thr		
				645					650					655			
Ile	Leu	Arg	Gly	Thr	Glu	Glu	Lys	Cys	Gly	Ser	Pro	Arg	Val	Arg	Thr		
			660					665					670				
Leu	Ser	Gly	Ser	Arg	Pro	Pro	Leu	Leu	Arg	Pro	Leu	Ser	Glu	Asn	Ser		
		675					680					685					
Gly	Asp	Glu	Asn	Met	Ser	Asp	Val	Thr	Phe	Asp	Ser	Leu	Pro	Ser	Ser		
	690					695					700						
Pro	Ser	Ser	Ala	Thr	Pro	His	Ser	Gln	Lys	Leu	Asp	His	Leu	His	Trp		
705					710						715				720		
Pro	Val	Phe	Ser	Asp	Leu	Asp	Asn	Met	Ala	Ser	Arg	Asp	His	Asp	His		
				725					730					735			
Leu	Asp	Asn	His	Arg	Glu	Ser	Glu	Asn	Ser	Gly	Asp	Ser	Gly	Tyr	Pro		
			740					745					750				
Ser	Glu	Lys	Arg	Gly	Glu	Leu	Asp	Asp	Pro	Glu	Pro	Arg	Glu	His	Gly		
		755					760					765					
His	Ser	Tyr	Ser	Asn	Arg	Lys	Tyr	Glu	Ser	Asp	Glu	Asp	Ser	Leu	Gly		
	770					775					780						
Ser	Ser	Gly	Arg	Val	Cys	Val	Glu	Lys	Trp	Asn	Leu	Leu	Asn	Ser	Ser		
785					790					795					800		
Arg	Leu	His	Leu	Pro	Arg	Ala	Ser	Ala	Val	Ala	Leu	Glu	Val	Gln	Arg		
				805					810					815			
Leu	Asn	Ala	Leu	Asp	Leu	Glu	Lys	Lys	Ile	Gly	Lys	Ser	Ile	Leu	Gly		
		820						825					830				
Lys	Val	His	Leu	Ala	Met	Val	Arg	Tyr	His	Glu	Gly	Gly	Arg	Phe	Cys		
		835					840					845					
Glu	Lys	Gly	Glu	Glu	Trp	Asp	Gln	Glu	Ser	Ala	Val	Phe	His	Leu	Glu		
	850					855					860						
His	Ala	Ala	Asn	Leu	Gly	Glu	Leu	Glu	Ala	Ile	Val	Gly	Leu	Gly	Leu		
865					870					875					880		
Met	Tyr	Ser	Gln	Leu	Pro	His	His	Ile	Leu	Ala	Asp	Val	Ser	Leu	Lys		
				885					890					895			
Glu	Thr	Glu	Glu	Asn	Lys	Thr	Lys	Gly	Phe	Asp	Tyr	Leu	Leu	Lys	Ala		
			900					905					910				
Ala	Glu	Ala	Gly	Asp	Arg	Gln	Ser	Met	Ile	Leu	Val	Ala	Arg	Ala	Phe		
		915					920					925					
Asp	Ser	Gly	Gln	Asn	Leu	Ser	Pro	Asp	Arg	Cys	Gln	Asp	Trp	Leu	Glu		
	930					935					940						
Ala	Leu	His	Trp	Tyr	Asn	Thr	Ala	Leu	Glu	Met	Thr	Asp	Cys	Asp	Glu		
945					950					955					960		
Gly	Gly	Glu	Tyr	Asp	Gly	Met	Gln	Asp	Glu	Pro	Arg	Tyr	Met	Met	Leu		
				965					970					975			
Ala	Arg	Glu	Ala	Glu	Met	Leu	Phe	Thr	Gly	Gly	Tyr	Gly	Leu	Glu	Lys		
			980					985					990				
Asp	Pro	Gln	Arg	Ser	Gly	Asp	Leu	Tyr	Thr	Gln	Ala	Ala	Glu	Ala	Ala		
		995					1000						1005				

Met Glu Ala Met Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys Ala
1010 1015 1020
Glu Glu Ala Trp Ala Gln Met Glu Glu
1025 1030

<210> 7
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
linker

<400> 7
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 8
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: c-Myc epitope

<400> 8
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 9
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: motif in
domain IX of kinases

<220>
<221> VARIANT
<222> (2)
<223> any amino acid

<220>
<221> VARIANT
<222> (4)..(5)
<223> any amino acid

<400> 9
Asp Xaa Trp Xaa Xaa Gly
1 5